SUPPLEMENTARTY MATERIAL

Outer retina micro-inflammation is driven by T cell responses prior to retinal degeneration in early age-related macular degeneration

Authors: Lucas Stürzbecher^{1,2,3,4}, Hendrik Bartolomaeus^{2,3,5,6}, Theda U. P. Bartolomaeus^{2,3,5,8}, Sylvia Bolz⁹, Andjela Sekulic¹, Marius Ueffing^{9,10}, Simon J. Clark^{9,10,11}, Nadine Reichhart¹, Sergio Crespo-Garcia⁷, Nicola Wilck^{2,3,5,12}, Olaf Strauß^{1,*}

Affiliations:

¹Experimental Ophthalmology, Department of Ophthalmology, Charité - Universitätsmedizin Berlin, Corporate Member of Freie Universität and Humboldt Universität zu Berlin, Berlin, Germany.

²Experimental and Clinical Research Center, a cooperation of Charité-Universitätsmedizin Berlin and Max-Delbrück-Center for Molecular Medicine, Berlin, Germany.

³Max-Delbrück-Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany.

⁴Eye Center, Medical Center, Faculty of Medicine, University Medical Center Freiburg, Freiburg, Germany.

⁵DZHK (German Centre for Cardiovascular Research), partner site Berlin, Berlin, Germany.

⁶Institute of Experimental Biomedicine, University Hospital Würzburg, Würzburg, Germany.

⁷École d'optométrie, University of Montreal, Montréal, Canada.

⁸Charité-Universitätsmedizin Berlin, corporate member of Freie Universität Berlin and Humboldt-Universität zu Berlin, Berlin, Germany.

⁹Institute for Ophthalmic Research, Department for Ophthalmology, Eberhard Karls University of Tübingen, Tübingen, Germany.

¹⁰Department for Ophthalmology, University Eye Clinic, Eberhard Karls University of Tübingen, Tübingen, Germany.

¹¹Lydia Becker Institute of Immunology and Inflammation, Faculty of Biology, Medicine, and Health, University of Manchester, Manchester, UK.

¹²Charité - Universitätsmedizin Berlin, corporate member of Freie Universität Berlin and Humboldt-Universität zu Berlin, Department of Nephrology and Internal Intensive Care Medicine, Berlin, Germany.

***Correspondence to**: Olaf Strauß, Experimental Ophthalmology, Charité Universitätsmedizin Berlin, Campus Virchow, Augustenburger Platz 1, 13353 Berlin, Germany, phone: +49 30 450 654 359, e-mail: <u>olaf.strauss@charite.de</u>

List of supplementary material

Supplementary detailed methods

Histology of human AMD samples.

Histological evaluation of murine RPE-choroid complex whole-mounts.

Immune cell phenotyping using multi-color flow cytometry.

Quantitative real-time PCR of ocular and splenic tissues.

Supplementary figures

Supplementary Figure S1. Gating strategy for splenic immune cells.

Supplementary Figure S2. Gating strategy for retinal immune cells.

Supplementary Figure S3. Retinal and splenic immune populations.

Supplementary Figure S4. Systemic activation von CD8⁺ and CD4⁺ T cells and effector memory T cells.

Supplementary Figure S5. Principal component analysis of splenic immune cells stratified by timepoint.

Supplementary Figure S6. No relevant shift due to autofluorescence in *Cx3cr1* animals in FITC channel.

Supplementary tables

Supplementary Table S1. List of human specimens.

Supplementary Table S2. Flowcytometric Reagents.

Supplementary Table S3. Histological Reagents.

Supplementary Table S4. Genes and Primers for qPCR.

Supplementary detailed methods

Histology of human AMD samples.

The sagittal sections were thawed at room temperature, permeabilized with 0.3% Triton X-100 in PBS and treated with the True Black Lipofuscin Autofluorescence quencher reagent (Linaris, 23007) to reduce autofluorescence. Tissue was incubated with primary antibodies CD3 (Roche/Ventana, 790-4341, 0,4µg/ml) and CD45R0 (DAKO, M0742, 1:100) for 16 hours at 4°C. After washing, tissues were incubated with secondary antibodies for 1 hour at room temperature and counterstained with DAPI (Thermo Scientific, 62248). Images were obtained using a Leica TCS SPE confocal microscope (Leica Microsystems GmbH, Wetzlar, Germany). CD3+CD45R0+ cells were counted per high power fields (HPF) at a magnification of 40x and analyzed using Leica Application Suite X Software and *ImageJ* (https://imagej.net/ij/). A detailed list of the antibodies used in this study is available in **Supplementary Table S2**.

Histological evaluation of murine RPE-choroid complex whole-mounts.

After enucleation and dissection of fat, muscles and connective tissue around the bulbus, eye globes were kept in 4% paraformaldehyde for 12 minutes. For whole-mount preparation, a circumferential incision behind the limbus was performed, and the cornea, Iens and ciliary body were discarded. Four to five radial incisions eased to flatten the whole-mount. The neuro-retina was lifted via cutting the opticus, and the remaining RPE-choroid complex was kept for histological evaluation. For ideal antibody penetration, tissue was permeabilized in TBS with 5% Triton X-100 for 24 hours at 4°C. After washing three times in TBS for 10 minutes, samples were subjected to blocking buffer (TBS with 5% BSA) for 60 minutes. Different primary antibodies were incubated for 48 hours at 4°C. RPE-choroid complexes were stained with anti-CD3 (1:100) and Acti-stain[™] Phalloidin (1:250), and signal was retrieved with secondary antibodies anti-rabbit (1:250) in DAPI working solution (300nM) for 60 minutes at room temperature. A detailed list of antibodies is provided in **Supplementary Table S2**. Tissues were whole-mounted with Fluorescence Mounting Medium (Dako) and imaged using a Leica TCS SP8 DLS confocal microscope (Leica Microsystems GmbH, Wetzlar, Germany). Further image analyses were performed using Leica Application Suit X Software and *ImageJ* (https://imagej.net/ij/).

Immune cell phenotyping using multi-color flow cytometry.

Following enucleation and dissection of fat, muscles, connective tissue, remaining N. opticus, cornea, lens and ciliary body the neuroretina-RPE-choroid-complex was digested for 30 min in a PBS TL Liberase solution at 37°C under constant movement and tissue was later mechanically homogenized with a gentle pipetting. The cellular suspension was then filtered through a 40µm-mesh strainer (Greiner Bio-one). To increase the yield of cells, each probe consisted of a pool of 3 eyes (2 animals).

For spleens, single cell suspensions of the organs were obtained through filtering through 70µmand 40µm-mesh strainers (Greiner Bio-one) applying mechanical pressure. Splenic suspensions were cleared through hypotonic erythrocyte lysis (155 mM NH4Cl, 10 mM NaHCO3, and 1 mM NaEDTA in water). Trypan blue was used to detect the yields of dead cells while counting. Each spleen (1 animal) was analyzed individually.

A probe sample of 10⁶ cells were used for multicolor flow cytometric analyses. All flow cytometric measurements included dead cell exclusion using Live/Dead Fixable Aqua Dead Cell Stain Kit. Cells were stained with surface antibodies (**Supplementary Table S3**) in PBS + 0.5 %BSA + 2 mM EDTA together with F_c blocking reagent (Miltenyi) for 30 min on ice. Data were recorded with a BD FACS LSR Fortessa and processed with the BD FACS Diva Software. Analyses were performed using FlowJo[™] Version 10.8.1 (BD). For immune cell analysis, Log transformation was used to normalize immune cell (features) counts. The gating strategies were set using Fluorescence Minus Ones Controls (FMOs) and are provided in **Supplementary Figure S1** and **Supplementary Figure S2**.

Quantitative real-time PCR of ocular and splenic tissues.

We determined gene expression in either RPE-choroid complexes or spleen. Upon excision, tissues were immediately snap frozen in liquid nitrogen and stored at -80°C. Total RNA was extracted with the RNeasy Mini Kit (QIAGEN) following the manufacturer's protocol, and concentration and quality measured with a NanoDrop-1000 Spectrophotometer (PeqLab). cDNA was synthesized from 300ng of RNA with the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems[™], Thermo Fisher). The expression of target genes was detected with either TaqMan or SYBR Green systems using the standard curve method on a QuantStudio[™] 3 software (Applied Biosystems[™], Thermo Fisher). The expression of target mRNA was normalized to the expression of the *18S* housekeeping gene. TaqMan primers were purchased whereas SYBR Green primers were designed in PrimerExpress 3.0 (Applied Biosystems) and synthetized by Biotez (Berlin, Germany). All primers, probes and sequences are provided in the **Supplementary Table S4**.

Supplementary figures



Supplementary Figure S1 Gating strategy for splenic immune cells

Figure S1. (A) Showing general gating strategy for splenic immune cells. **(B)** Gating strategy for T cells from which Treg-like (CD25⁺), Th17-like (CD196⁺), CD69⁺ and KLRG1⁺ cells were determined, as well as T memory cell populations. **(C)** for non T cells.



Supplementary Figure S2 Gating strategy for retinal immune cells

Figure S2. (A) Showing general gating strategy for retinal immune cells. **(B)** Gating strategy for T cells from which Treg-like (CD25⁺), Th17-like (CD196⁺), CD69⁺ and KLRG1⁺ cells were determined, as well as T memory cell populations. **(C)** for non T cells, inflammatory microglia and monocytes/macrophages respectively.



Supplementary Figure S3 Retinal and spenic immune populations

Figure S3. (A) Retinal TCRgd and non T cell immune populations. (B) Splenic TCRgd and non T cell immune populations. (C) KLRG-1 and CD69 marker expression on splenic CD4⁺ regulatory T cells. (D) KLRG-1 and CD69 marker expression on splenic CD4⁺ and CD8⁺ Th17 like cells. (E) Splenic CD4⁺ tissue-resident memory T cells. Tested with double sided t-test or Mann-Whitney U test. *P < 0.05; **P < 0.01; ***P < 0.001; ****P < 0.001.



Figure S4. (A, C) Representative gates for KLRG1 and CD69 and CD44 and CD62L on splenic CD8⁺ T cells. Numbers representing percentage of gated immune cells. (E, G) Same for splenic CD4⁺ T cells. (B, D, F, H) Quantification of marker expression in (B) CD8⁺ T cell population (D) CD8⁺ effector memory T cell population (CD44⁺ CD62L⁻) (F) CD4⁺ T cell population and (H) CD4⁺ effector memory T cell population (CD44⁺ CD62L⁻). Tested with double sided t-test or Mann-Whitney U test. *P < 0.05; **P < 0.01; ***P < 0.001; ****P < 0.0001. 8M WT and 12M KO n = 12; 12M WT and 8M KO n = 10.

Supplementary Figure S5 Principal component analysis of splenic immune cells stratified by timepoint



Figure S5. (A, B) Principal component analysis (PCA) of splenic immune cells. Each triangle represents a single animal. Saturated symbol represents mean of a group. (A) shows C57bl6/j (B) Cx3cr1 animals, respective coloring indicates timepoint. (C) shows the 12 most contributing immune cell populations to dim2.

Sample Background Count 12 month wild type, spleen C57bl6/j 10000 1,5K 12 month knockout,spleen Cx3cr1^{gfp/gfp} 10000 Count 1,0K 500 0 10⁵ 10³ -10³ -10⁴ 0 Comp-FITC-A

Supplementary Figure S6 No relevant shift due to autofluorescence in Cx3cr1 mice in FITC chanel A

Figure S6. (A) Showing FITC signal of unstained splenic cells from C57bl6/j (light blue) and Cx3cr1 (orange) mice. Histogramm showing no relevant shift of green autofluerencence in FITC chanel from $Cx3cr1^{gfp/gfp}$ knockout.

Supplementary Tables

| Control | | | Early AMD | | | Late AMD | | |
|---------|-----|-------------|-----------|-----|-------------|----------|-----|-------------|
| ID | Sex | Age (years) | ID | Sex | Age (years) | ID | Sex | Age (years) |
| ETR104 | Μ | 68 | ETR216 | М | 79 | ETR64 | М | 69 |
| ETR65 | Μ | 79 | ETR631 | F | 71 | ETR405 | М | 80 |
| ETR314 | F | 71 | | | | ETR292 | F | 72 |
| Average | | 72.6 ± 5.68 | Average | | 72.6 ± 5.68 | Average | | 73.6 ± 5.68 |

Supplementary Table S1. List of human specimens

AMD: Age-related macular degeneration; ETR: Eye tissue resource; M: male; F: female

Supplementary Table S2. Flowcytometric Reagents

| Antibody | Fluorophore | Clone | Identifier | Source | Concentration |
|--------------------------|--------------------|--------|-------------|------------------|---------------|
| Fc Blocking | | | 130-092-575 | Milteny Biotech | 1:100 |
| CD3 – | BV421 | 17A2 | 564008 | BD Horizon | 1:50 |
| CD4 – | APC Vio770 | GK1.5 | 130-118-957 | Milteny Biotech | 1:100 |
| CD8 – | PerCP Cy5.5 | 53-6.7 | 551162 | BD Pharmingen | 1:100 |
| CD11b – | Alexa Fluor 700 | M1/70 | 557960 | BD Pharmingen | 1:100 |
| CD25 – | PE CF594 | PC61 | 562694 | BD Horizon | 1:100 |
| CD44 – | FITC | IM7 | 553133 | BD Pharmingen | 1:100 |
| CD45 – | PE Vio770 | REA737 | 130-110-661 | Miltenyi Biotech | 1:100 |
| CD 62L – | APC | MEL-14 | 553152 | BD Pharmingen | 1:100 |
| CD69 – | PE Cy5 | H1.2F3 | 104510 | BioLegend | 1:100 |
| CD103 – | BV650 | 2E7 | 748256 | BD OptiBuild | 1:50 |
| CD196 – | BV711 | 11A9 | 563923 | BD Horizon | 1:100 |
| KLRG1 – | BV786 | 2F1 | 565477 | BD Horizon | 1:100 |
| Ly6C – | BV605 | AL21 | 563011 | BD Horizon | 1:100 |
| TCRgd | PE – CF592 | GL3 | 553178 | BD Pharmingen | 1:100 |
| Live/ Dead- | Aqua 405 | | L34957 | Thermo Fischer | 1:1000 |
| Buffer – | | | BD 566349 | BD Biosciences | |
| BD Horizon™ | | | | | |
| Brilliant Stain | | | | | |
| Buffer | | | | | |
| Liberase [™] TL | | | 05401020001 | Roche | 0,8 U/mL |

Supplementary Table S3. Histological Reagents

| Antibody/Reagent | Clone | Identifier | Source |
|-----------------------------|-------|------------|--------------------------|
| Anti-CD3 | SP7 | ab16669 | Abcam |
| Anti-CD3 | | 790-4341 | Roche/Ventana |
| Anti-CD45-R0 | | M0742 | DAKO |
| Acti-stainTM 555 Phalloidin | | PHDH1 | Cytoskeleton |
| Isolectin GS-IB4 AFTM 568 | | l21412 | Thermo Fischer Scientifc |
| Conjugate | | | |

| Goat anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor™ 488 | A11034 | Invitrogen |
|--|-------------|------------------------------|
| Goat anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor™ 568 | A11031 | Invitrogen |
| Alexa-Fluor® 647 -AffiniPure Donkey Anti-Rabbit IgG (H+L) | 711-605-152 | Dianova |
| DAPI (for murine stainings) | 10236276001 | Roche |
| DAPI (for human stainings) | 62248 | Thermo Scientific |
| Dako Flourescence Mounting Medium | S3032 | Agilent Technologies |
| Paraformaldehyd 16% Aqueous solution EM grade | 15710 | Electron Microscopy Sciences |

Supplementary Table S4. Genes and Primers for qPCR

| Gana | | | | |
|--------------|----------------------------------|--|--|--|
| | complement component 3 | Mm00/37858 m1 | | |
| Cfh | complement component facto | nin00407000_nin nr h Mm01200248 m1 | | |
| Ctla2a | | Mm00484032 a1 | | |
| Gliaza | associated protein 2 alpha | MI1100404032_g1 | | |
| Foxn3 | forkhead box P3 | Mm00475162 m1 | | |
| Icam1 | intercellular adhesion molecu | Mm00516023 m1 | | |
| 110 | interleukin 10 | Mm01288386 m1 | | |
| 1115 | interleukin 15 | Mm00434210 m1 | | |
| II17a | interleukin 17A | Mm00439618 m1 | | |
| ll1b | interleukin 1 beta | Mm00434228 m1 | | |
| 112 | interleukin 2 | Mm00434256 m1 | | |
| 1122 | interleukin 22 | Mm01226722 g1 | | |
| ll23a | interleukin 23 | Mm00518984 m1 | | |
| <i>l</i> /6 | interleukin 6 | Mm00446190 m1 | | |
| <i> 7</i> | interleukin 7 | Mm01295803 m1 | | |
| ltgb2 | integrin beta 2 | Mm00434513 m1 | | |
| Rbp3 | retinol binding protein 3 | Mm01220858 m1 | | |
| Design | ed primers (all synthesized by l | Biotez, Berlin, Germany) | | |
| Gene | Gene name | Sequences | | |
| 18s | 18s ribosomal 1 | F: ACA TCC AAG GAA GGC AGC AG | | |
| | | R: TTT TCG TCA CTA CCT CCC CG | | |
| | | Probe: 6-FAM CGC GCA AAT | | |
| Ccl2 | C-C motif chemokine | F: GGC TCA GCC AGA TGC AGT TAA | | |
| | ligand 2 | R: CCT ACT CAT TGG GAT CAT CTT GCT | | |
| | | Probe: CCC CAC TCA CCT GCT GCT ACT CAT TCA | | |
| Ccl5 | C-C motif chemokine | F: GCA GTC GTG TTT GTCACT CGA A | | |
| | ligand 5 | R: GAT GTA TTC TTG AAC CCA CTT CTT CTC | | |
| | | Probe: FAM-AAC CGC CAA GTG TGT GCC AAC CC-TAMRA | | |
| Cxcl1 | C-X-C motif chemokine | F: CTG CAC CCA AAC CGA AGT C | | |
| | ligand 1 | R: AGC TTC AGG GTC AAG GCA AG | | |
| 114 | interleukin 4 | F: GGC ATT TTG AAC GAG GTC ACA | | |
| | | R: GAC GTT TGG CAC ATC CAT CTC | | |
| Pgf | placental growth factor | F: TGG TGC CTT TCA ACG AAG TG | | |
| | | CAT CCA AGA TGT ACA CCA GCT TCT | | |
| | | Probe: FAM- TCG CAG CTA CTG TCG GCC CAT G | | |
| Icrb | I cell receptor beta | F: GGC ACA ACT CTC GAA ACC A | | |
| | | R: CCA CTT GTC CTC CTC TGA AAG C | | |
| T C 4 | | Prope: FAM-TCC CGC TGC CAA GTG CAG TTC CA-TAMRA | | |
| I gfb1 | transforming growth factor | F: CCC GAA GCG GAC TAC TAT GC | | |
| Tuf | | K: IAG ATG GCG TTG TTG CGG T | | |
| Int | tumor necrosis factor | F: GGT CCC CAA AGG GAT GAG AA | | |
| | | K: TGA GGG TCT GGG CCA TAG AA | | |
| | | I PTODE: FAM-LLC CCA AAL GGC CTC CCT CTC ATC A-TAMRA | | |